

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

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Technical Assistance.....703-287-0200

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PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

<110>
 <120>
 <130>
 <140>
 <141>
 <160>

MANDATORY ~~sequence identifier and~~ *response needed for a U.S. filing*
 delete

09/214881

Since the U.S.
 filing date was after
 July 1, 1998, this format
 Does Not Comply is invalid
 Corrected Diskette Needed

please ensure all
 amino acid numbers are
 aligned under every
 5 amino acids. Do NOT
 use TAB code between
 amino acids

Please
 follow format
 shown in

attached sample
 sequence listing.

Many responses
 are no longer
 used under the
 new sequence rules.

Please consult
 new sequence rules
 for valid format.

SEQUENCE LISTING

<210> ~~SEQ ID NO: 1~~
 <211> ~~LENGTH: 214~~
 <212> ~~TYPE: amino acid~~ PRT > <213> Human
 <220> ~~MOLECULAR TYPE: Peptide~~
 <223> ~~FEATURE: FHM-1~~
 <223> ~~ORIGINAL SOURCE: Human~~
 <400> ~~SEQUENCE 1~~
 Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn
 20 25 30 35
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys
 40 45 50
 Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg
 55 60 65 70
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp
 75 80 85 90
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr
 95 100 105
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
 110 115 120 125
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro Tyr Glu
 130 135 140
 Lys Lys Ala Ala Lys Leu Lys Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
 145 150 155 160
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser
 165 170 175 180
 Lys Lys Lys Lys Glu Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu
 185 190 195
 Glu Glu Asp Glu Glu Asp Glu Asp Glu Glu Glu Asp Asp Asp Asp Glu
 200 205 210

<210> ~~SEQ ID NO: 2~~
 <211> ~~LENGTH: 208~~
 <212> ~~TYPE: amino acid~~ PRT > <213> Human
 <220> ~~MOLECULAR TYPE: Peptide~~
 <223> ~~FEATURE: FHM-2~~
 <223> ~~ORIGINAL SOURCE: Human~~
 <400> ~~SEQUENCE 2~~
 Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn
 20 25 30 35
 Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys
 40 45 50
 Glu Lys Ser Lys Phe Glu Asp Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg
 55 60 65 70
 Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp
 75 80 85 90
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His
 95 100 105
 Arg Pro Lys Ile Lys Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
 110 115 120 125
 Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu

Please review the
 Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
 <223> fields of each sequence which presents at least one n or Xaa.

130 135 140
 Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
 145 150 155 160
 Ala Lys Gly Lys Ser Glu Ala Gly Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser
 165 170 175 180
 Lys Lys Lys Asn Glu Pro Glu Asp Glu Glu Glu Glu Glu Glu Asp Glu
 185 190 195
 Asp Glu Glu Glu Glu Asp Glu Asp Glu Glu
 200 205

SEQ ID NO F,R
 LENGTH F214
 TYPE Famino acid
 MOLECULAR TYPE Fpeptide
 FEATURE FHMG-1
 ORIGINAL SOURCE FBovine
 SEQUENCE

Edti

delete

Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
 @@@@ 5 10 15
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn
 20 25 30 35
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys
 40 45 50
 Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg
 55 60 65 70
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp
 75 80 85 90
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr
 95 100 105
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
 110 115 120 125
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys Gln Pro Tyr Glu
 130 135 140
 Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
 145 150 155 160
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser
 165 170 175 180
 Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu
 185 190 195
 Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Asp Asp Asp Glu
 200 205 210

SEQ ID NO F,S
 LENGTH F214
 TYPE Famino acid
 MOLECULAR TYPE Fpeptide
 FEATURE FHMG-1
 ORIGINAL SOURCE FPorcine
 SEQUENCE

Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn
 20 25 30 35
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys
 40 45 50

Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg
 55 60 65 70
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp
 75 80 85 90
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr
 95 100 105
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
 110 115 120 125
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys His Pro Tyr Glu
 130 135 140
 Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
 145 150 155 160
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser
 165 170 175 180
 Lys Lys Lys Lys Glu Glu Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu
 185 190 195
 Glu Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Asp Asp Glu
 200 205 210

SEQ ID NO F,T
 LENGTH F214
 TYPE Famino acid
 MOLECULAR TYPE Fpeptide
 FEATURE FHMG-1
 ORIGINAL SOURCE FRat
 SEQUENCE

Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn
 20 25 30 35
 Phe Ser Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys
 40 45 50
 Glu Lys Gly Lys Phe Glu Asp Met Ala Lys Ala Asp Lys Ala Arg Tyr Glu Arg
 55 60 65 70
 Glu Met Lys Thr Tyr Ile Pro Pro Lys Gly Glu Thr Lys Lys Lys Phe Lys Asp
 75 80 85 90
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu Tyr
 95 100 105
 Arg Pro Lys Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
 110 115 120 125
 Lys Leu Gly Glu Met Trp Asn Asn Thr Ala Ala Asp Asp Lys His Pro Tyr Glu
 130 135 140
 Lys Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
 145 150 155 160
 Ala Lys Gly Lys Pro Asp Ala Ala Lys Lys Gly Val Val Lys Ala Glu Lys Ser
 165 170 175 180
 Lys Lys Lys Lys Glu Glu Glu Asp Asp Glu Glu Asp Glu Glu Asp Glu Glu Glu
 185 190 195
 Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Glu Asp Asp Asp Asp Glu
 200 205 210

SEQ ID NO F,U
 LENGTH F209
 TYPE Famino acid
 MOLECULAR TYPE Fpeptide

FEATURE FHMG-2

ORIGINAL SOURCE FPorcine

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
5 10 15
Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn
20 25 30 35
Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys
40 45 50
Glu Lys Ser Lys Phe Glu Asp Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg
55 60 65 70
Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp
75 80 85 90
Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His
95 100 105
Arg Pro Lys Ile Lys Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
110 115 120 125
Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu
130 135 140
Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
145 150 155 160
Ala Lys Gly Lys Gly Glu Ala Gly Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser
165 170 175 180
Lys Lys Lys Asn Glu Pro Glu Asp Glu Glu Glu Glu Glu Glu Glu Asp
185 190 195
Glu Asp Glu Glu Glu Glu Asp Glu Asp Glu Glu
200 205

SEQ ID NO F,V

LENGTH F186

TYPE Famino acid

FEATURE Fpeptide

FEATURE Fpartial sequence of HMG-2

ORIGINAL SOURCE FBovine

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
5 10 15
Val Gln Thr Ser Arg Glu Glu His Lys Lys Lys His Pro Asp Ala Ser Val Asn
20 25 30 35
Phe Ser Glu/Arg Trp Lys Thr Met Ser Ala Lys Glu Lys Ser Lys Phe Glu Asp
40 45 50
Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg Glu Met Lys Asn Tyr Val Pro
55 60 65 70
Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp Pro Asn Ala Pro Lys Arg Pro
75 80 85 90
Pro Ser Ala Phe Phe Leu Phe Ser Ala Glu His Arg Pro Lys Ile Lys Ala Glu
95 100 105
His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys Lys Leu Gly Glu Met Trp Ser
110 115 120 125
Gln Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu Gln Lys Ala Ser Lys Leu Lys
130 135 140
Glu Lys Tyr Glu Lys Xaa Ala Ala Tyr Arg Ala Lys Gly Lys Ser Glu Ala Gly
145 150 155 160
Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser Lys Lys Lys Asn Glu Pro Glu Asp
165 170 175 180

Glu Glu Glu Glu Glu Glu
185

SEQ ID NO F,W

LENGTH F209

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FEATURE FHMg-2

ORIGINAL SOURCE FRat

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
5 10 15
Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn
20 25 30 35
Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ala Lys
40 45 50
Glu Lys Ser Lys Phe Glu Asp Met Ala Lys Ser Asp Lys Ala Arg Tyr Asp Arg
55 60 65 70
Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp
75 80 85 90
Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His
95 100 105
Arg Pro Lys Ile Lys Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
110 115 120 125
Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu
130 135 140
Gln Lys Ala Ala Lys Leu Lys Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
145 150 155 160
Ala Lys Gly Lys Ser Glu Val Gly Lys Lys Gly Pro Gly Arg Pro Thr Gly Ser
165 170 175 180
Lys Lys Lys Asn Glu Pro Glu Asp Glu Glu Glu Glu Glu Glu Asp Asp
185 190 195
Glu Asp Glu Glu Glu Glu Asp Glu Asp Glu Glu
200 205

SEQ ID NO F,X

LENGTH F206

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FEATURE FHMg-2

ORIGINAL SOURCE FChicken

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Tyr Phe
5 10 15
Val Gln Thr Cys Pro Arg Glu His Lys Lys Lys His Pro Asp Ser Ser Val Asn
20 25 30 35
Phe Ala Glu Phe Ser Arg Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ser Lys
40 45 50
Glu Lys Gly Lys Phe Glu Glu Met Ala Lys Gly Asp Lys Ala Arg Tyr Asp Arg
55 60 65 70
Glu Met Lys Asn Tyr Val Pro Pro Lys Gly Glu Lys Lys Gly Lys Lys Lys Asp
75 80 85 90
Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Phe Leu Phe Cys Ser Glu His
95 100 105
Arg Pro Lys Ile Lys Asn Asp His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys

110 115 120 125
 Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Asp Lys Gln Pro Tyr Glu
 130 135 140
 Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Ile Ala Ala Tyr Arg
 145 150 155 160
 Ala Lys Ser Lys Ser Asp Ala Gly Lys Lys Gly Pro Gly Arg Pro Ala Gly Ser
 165 170 175 180
 Lys Lys Lys Ala Glu Pro Glu Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu
 185 190 195
 Glu Glu Glu Glu Glu Asp Glu Glu
 200 205

SEQ ID NO F,P,O

LENGTH F201

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FEATURE FHMG-2a 

ORIGINAL SOURCE FChicken

SEQUENCE

Ala Lys Gly Asp Pro Lys Lys Pro Lys Gly Lys Met Ser Ala Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Asn Pro Glu Val Pro Val Asn
 20 25 30 35
 Phe Ala Glu Phe Ser Lys Lys Cys Ser Glu Arg Trp Lys Thr Met Ser Ser Lys
 40 45 50
 Glu Lys Ala Lys Phe Asp Glu Met Ala Lys Ala Asp Lys Val Arg Tyr Asp Arg
 55 60 65 70
 Glu Met Lys Asp Tyr Gly Pro Ala Lys Gly Gly Lys Lys Lys Lys Asp Pro Asn
 75 80 85 90
 Ala Pro Lys Arg Pro Pro Ser Gly Phe Phe Leu Phe Cys Ser Glu Phe Arg Pro
 95 100 105
 Lys Ile Lys Ser Thr Asn Pro Gly Ile Ser Ile Gly Asp Val Ala Lys Lys Leu
 110 115 120 125
 Gly Glu Met Trp Asn Asn Leu Ser Asp Gly Glu Lys Gln Pro Tyr Asn Asn Lys
 130 135 140
 Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Val Ala Asp Tyr Lys Ser Lys
 145 150 155 160
 Gly Lys Phe Asp Gly Ala Lys Gly Ala Ala Thr Lys Ala Ala Arg Lys Lys Val
 165 170 175 180
 Glu Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Asp Glu Asp Asp
 185 190 195
 Asp Asp Glu
 200

SEQ ID NO F,P,P

LENGTH F208

TYPE Famino acid

MOLECULAR TYPE Fpeptide

ORIGINAL SOURCE FMouse

FEATURE FHMG-2

SEQUENCE

Gly Lys Gly Asp Pro Ile Lys Pro Leu Gly Lys Met Ser Ser Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Cys Arg Glu Glu His Lys Lys Lys His Pro Asn Ser Ser Val Asn
 20 25 30 35

Phe Ala Glu Ile Ser Lys Lys Cys Ser Lys Arg Trp Lys Thr Met Ser Ala Lys
 40 45 50
 Glu Asn Ser Lys Phe Glu Asp Leu Ala Lys Ser Asp Lys Ala Cys Tyr Tyr Arg
 55 60 65 70
 Glu Met Lys Asn Tyr Val Ser Pro Lys Gly Asp Lys Lys Gly Lys Lys Lys Asp
 75 80 85 90
 Pro Asn Ala Pro Lys Arg Pro Pro Ser Ala Phe Cys Leu Phe Cys Ser Glu Asn
 95 100 105
 Arg Pro Lys Ile Lys Ile Glu Tyr Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
 110 115 120 125
 Lys Leu Gly Glu Met Trp Ser Glu Gln Ser Ala Lys Glu Lys Gln Pro Tyr Glu
 130 135 140
 Gln Lys Ala Ala Lys Leu Lys Glu Lys Tyr Glu Lys Asp Phe Ala Ala Tyr Arg 145 150
 155 160
 Val Lys Gly Lys Ser Glu Ala Gly Lys Lys Gly Pro Gly Arg Pro Ala Gly Ser 165 170
 175 180
 Lys Lys Lys Asn Asp Ser Glu Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu 185 190
 195
 Asp Glu Glu Gly Glu Glu Glu Asp Glu Glu
 200 205

SEQ ID NO F,P,Q

LENGTH F32

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FRAGMENT TYPE FN-terminal fragment of 28KDa

ORIGINAL SOURCE

CELL TYPE Fneutrophil-type cell derived from promyelocytic leukemia

CELL LINE Fneutrophil-type cell line (ATCC CCL-240)

FEATURE

IDENTIFICATION METHOD F,d

SEQUENCE

Gly Lys Gly Asp Pro Asn Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Xaa Arg Glu Glu His Lys Lys Lys His Pro Asp
 20 25 30

SEQ ID NO F,P,R

LENGTH F32

TYPE Famino acid

MOLECULAR TYPE Fpeptide

FRAGMENT TYPE FN-terminal fragment of 29KDa

ORIGINAL SOURCE

CELL TYPE Fneutrophil-type cell derived from promyelocytic leukemia

CELL LINE Fneutrophil-type cell line (ATCC CCL-240)

FEATURE

IDENTIFICATION METHOD F,d

SEQUENCE

Gly Lys Gly Asp Pro Lys Lys Pro Arg Gly Lys Met Ser Ser Tyr Ala Phe Phe
 5 10 15
 Val Gln Thr Xaa Arg Glu Glu His Lys Lys Lys His Pro Asp
 20 25 30

KA016

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